CLAIMS

What is claimed is:

1. A method of modulating angiogenesis at a site, the method comprising causing an effective amount of a composition comprising a BTL.012-like protein to be supplied to the site.

2. The method of claim 1 wherein the BTL.012-like protein has an amino acid sequence identical to SEQ ID NO:1.

3. The method of claim 1 wherein the BTL.012-like protein has an amino acid sequence which is at least 60% identical over at least 40 residues to SEQ ID NO:1.

4. The method of claim 1 wherein the BTL.012-like protein has an amino acid sequence which is at least 70% identical over at least 30 residues to SEQ ID NO:1.

5. A method of modulating the formation of cells into capillary-like structures comprising contacting the cells with a biologically effective amount of a composition comprising a BTL.012-like protein.

6. The method of claim 5 wherein the cells are endothelial cells of human origin.

7. A protein characterized by having a deduced amino acid sequence which is at least 60% identical over 40 residues to SEQ ID NO:1.

8. The protein according to claim 7, wherein the deduced amino acid sequence is at least 80% identical over 50 residues to SEQ ID NO:1.

9. A pharmaceutical composition for modulating angiogenesis comprising a protein characterized by having a deduced amino acid sequence which is at least 60% identical over 40 residues to SEQ ID NO:1 and a pharmaceutically acceptable carrier.

10. The method of claim 1, wherein the site is within a human patient and the protein is supplied to the site via a pharmaceutical composition according to claim 9.

11. The method of claim 10, wherein the site is within a human patient and the protein is supplied to the site via a process of gene therapy.

12. A method for preventing, treating, or ameliorating a medical condition in an individual, the method comprising providing a source of an effective amount of at least one protein according to claim 7 to the individual.

13. The method of claim 12, wherein the protein is supplied to the individual by providing to the individual a source of a polynucleotide encoding the protein and expressing the protein in vivo.

14. The method of claim 12, wherein the medical condition is selected from the group consisting of cancer, metastasis, diabetic retinopathy, macular degeneration, cardiovascular disease, and a wound.

15. A polynucleotide selected from the group consisting of (a) a polynucleotide coding for a protein according to claim 7; (b) a polynucleotide complementary to (a); (c) a polynucleotide having at least 90% identity over at least 20 bases to SEQ ID NO:34; and (d) a polynucleotide complementary to (c).

16. The polynucleotide according to claim 15, wherein the polynucleotide is operably linked within an expression vector to a promoter, the expression vector thus being capable of being used to express the protein according to claim 1.

17. A method for producing a protein according to claim 7 comprising the steps of
(a) introducing an expression vector capable of expressing the protein according to claim 7 into a cell capable of expressing the protein according to claim 7,
(b) growing cells resulting from step (a) under conditions sufficient to allow the cells to express the protein according to claim 7, and
(c) recovering the protein according to claim 7 from the result of step (b).

18. An antibody against a protein according to claim 7.

19. A method for diagnosing a disease or medical condition or susceptibility to a disease or medical condition, the disease or medical condition related to inadequate or excess expression of a protein according to claim 7, the method comprising the steps
(a) determining the level of expression of said protein in a sample; and
(b) comparing the level of expression of said protein against a standard to make a diagnosis.

20. The method of claim 19, wherein the medical condition is selected from the group consisting of cancer, metastasis, diabetic retinopathy, macular degeneration, cardiovascular disease, and a wound.

21. A protein characterized by having a deduced amino acid sequence which is at least 60% identical over 40 residues to SEQ ID NO:33.